



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/088,549
Source: PCTIO
Date Processed by STIC: 4/8/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

RE TIC

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 10/082,549

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220>
 Use of <220>
 Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



Does Not Comply
Information Needed

PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/088,549

DATE: 04/08/2002
TIME: 14:28:31

Input Set : A:\DEBE007US.txt
Output Set: N:\CRF3\04082002\J088549.raw

3 <110> APPLICANT: Erik Nielsen
 4 Savvas Chritophoridis
 5 Carol Murphy
 6 Marino Zerial
 7 Stefano De Renzis
 9 <120> TITLE OF INVENTION: ASSAY TO DETECT SUBSTANCES USEFUL FOR THERAPY
 11 <130> FILE REFERENCE: DEBE:007US
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/088,549
 14 <141> CURRENT FILING DATE: 2002-03-15
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP 00/09130
 17 <151> PRIOR FILING DATE: 2000-09-18
 19 <150> PRIOR APPLICATION NUMBER: EP 99 118 385.6
 20 <151> PRIOR FILING DATE: 1999-09-16
 22 <160> NUMBER OF SEQ ID NOS: 16
 24 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

647 <210> SEQ ID NO: 6
 648 <211> LENGTH: 784
 649 <212> TYPE: PRT
 650 <213> ORGANISM: Homo sapiens
 652 <400> SEQUENCE: 6
 653 Met Ala Ser Leu Asp Asp Pro Gly Glu Val Arg Glu Gly Phe Leu Cys
 654 1 5 10 15
 656 Pro Leu Cys Leu Lys Asp Leu Gln Ser Phe Tyr Gln Leu His Ser His
 657 20 25 30
 659 Tyr Glu Glu Glu His Ser Gly Glu Asp Arg Asp Val Lys Gly Gln Ile
 660 35 40 45
 662 Lys Ser Leu Val Gln Lys Ala Lys Lys Ala Asp Arg Leu Leu Lys
 663 50 55 60
 665 Arg Glu Gly Asp Asp Arg Ala Glu Ser Gly Thr Gln Gly Tyr Glu Ser
 666 65 70 75 80
 667 Phe Ser Tyr Gly Gly Val Asp Pro Tyr Met Trp Glu Pro Gln Glu Leu
 668 85 90 95
 670 Gly Ala Val Arg Ser His Leu Ser Asp Phe Lys Lys His Arg Ala Ala
 671 100 105 110
 673 Arg Ile Asp His Tyr Val Val Glu Val Asn Lys Leu Ile Ile Arg Leu
 674 115 120 125
 676 Glu Lys Leu Thr Ala Phe Asp Arg Thr Asn Thr Glu Ser Ala Lys Ile
 677 130 135 140
 679 Arg Ala Ile Glu Lys Ser Val Val Pro Trp Val Asn Asp Gln Asp Val

*X32 found in sequence, requires explanation
See error summary sheet item 3*

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680	145	150	155	160
682	Pro Phe Cys Pro Asp Cys Gly Asn Lys Phe Ser Ile Arg Asn Arg Arg			
683	165	170	175	
685	His His Cys Arg Leu Cys Gly Ser Ile Met Cys Lys Lys Cys Met Glu			
686	180	185	190	
688	Leu Ile Ser Leu Pro Leu Ala Asn Lys Leu Thr Ser Ala Ser Lys Glu			
689	195	200	205	
691	Ser Leu Ser Thr His Thr Ser Pro Ser Gln Ser Pro Asn Ser Val His			
692	210	215	220	
694	Gly Ser Arg Arg Gly Ser Ile Ser Ser Met Ser Ser Val Ser Ser Val			
695	225	230	235	240
697	Leu Asp Glu Lys Asp Asp Asp Arg Ile Arg Cys Cys Thr His Cys Lys			
698	245	250	255	
700	Asp Thr Leu Leu Lys Arg Glu Gln Gln Ile Asp Glu Lys Glu His Thr			
701	260	265	270	
703	Pro Asp Ile Val Lys Leu Tyr Glu Lys Leu Arg Leu Cys Met Glu Lys			
704	275	280	285	
706	Val Asp Gln Lys Ala Pro Glu Tyr Ile Arg Met Ala Ala Ser Leu Asn			
707	290	295	300	
709	Ala Gly Glu Thr Thr Tyr Ser Leu Glu His Ala Ser Asp Leu Arg Val			
710	305	310	315	320
711	Glu Val Gln Lys Val Tyr Glu Leu Ile Asp Ala Leu Ser Lys Lys Ile			
712	325	330	335	
714	Leu Thr Leu Gly Leu Asn Gln Asp Pro Pro Pro His Pro Ser Asn Leu			
715	340	345	350	
717	Arg Leu Gln Arg Met Ile Arg Tyr Ser Ala Thr Leu Phe Val Gln Glu			
718	355	360	365	
720	Lys Leu Leu Gly Leu Met Ser Leu Pro Thr Lys Glu Gln Phe Glu Glu			
721	370	375	380	
E-->	723 Leu Lys Lys Lys Arg Lys Glu Glu Met Glu Arg Lys Arg Xaa Val Glu			
724	385	390	395	400
726	Arg Gln Ala Ala Leu Glu Ser Gln Arg Arg Leu Glu Glu Arg Gln Ser			
727	405	410	415	
729	Gly Leu Ala Ser Arg Ala Ala Asn Gly Glu Val Ala Ser Leu Arg Arg			
730	420	425	430	
732	Gly Pro Ala Pro Leu Arg Lys Ala Glu Gly Trp Leu Pro Leu Ser Gly			
733	435	440	445	
735	Gly Gln Gly Gln Ser Glu Asp Ser Asp Pro Leu Leu Gln Gln Ile His			
736	450	455	460	
738	Asn Ile Thr Ser Phe Ile Arg Gln Ala Lys Ala Ala Gly Arg Met Asp			
739	465	470	475	480
E-->	741 Glu Val Arg Thr Leu Gln Glu Xaa Leu Arg Gln Leu Gln Asp Glu Tyr			
742	485	490	495	
744	Asp Gln Gln Gln Thr Glu Lys Ala Ile Glu Leu Ser Arg Arg Gln Ala			
745	500	505	510	
747	Glu Glu Glu Asp Leu Gln Arg Glu Gln Leu Gln Met Leu Arg Glu Arg			
748	515	520	525	
750	Glu Leu Glu Arg Glu Arg Glu Gln Phe Arg Val Ala Ser Leu His Thr			
751	530	535	540	

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753 Arg Thr Arg Ser Leu Asp Phe Arg Glu Ile Gly Pro Phe Gln Leu Glu
754 545 550 555 560
755 Pro Ser Arg Glu Pro Arg Thr His Leu Ala Tyr Ala Leu Asp Leu Gly
756 565 570 575
758 Ser Ser Pro Val Pro Ser Ser Thr Ala Pro Lys Thr Pro Ser Leu Ser
759 580 585 590
761 Ser Thr Gln Pro Thr Arg Val Trp Ser Gly Pro Pro Ala Val Gly Gln
762 595 600 605
764 Glu Arg Leu Pro Gln Ser Ser Met Pro Gln Gln His Glu Gly Pro Ser
765 610 615 620
767 Leu Asn Pro Phe Asp Glu Glu Asp Leu Ser Ser Pro Met Glu Glu Ala
768 625 630 635 640
770 Thr Thr Gly Pro Pro Ala Ala Gly Val Ser Leu Asp Pro Ser Ala Arg
771 645 650 655
773 Ile Leu Lys Glu Tyr Asn Pro Phe Glu Glu Asp Glu Glu Glu
774 660 665 670
776 Ala Val Ala Gly Asn Pro Phe Ile Gln Pro Asp Ser Pro Ala Pro Asn
777 675 680 685
779 Pro Phe Ser Glu Glu Asp Glu His Pro Gln Gln Arg Leu Ser Ser Pro
780 690 695 700
782 Leu Val Pro Gly Asn Pro Phe Glu Glu Pro Thr Cys Ile Asn Pro Phe
783 705 710 715 720
785 Glu Met Asp Ser Asp Ser Gly Pro Glu Ala Glu Glu Pro Ile Glu Glu
786 725 730 735
788 Glu Leu Leu Leu Gln Gln Ile Asp Asn Ile Lys Ala Tyr Ile Phe Asp
789 740 745 750
791 Ala Lys Gln Cys Gly Arg Leu Asp Glu Val Glu Val Leu Thr Glu Asn
792 755 760 765
794 Leu Arg Glu Leu Lys His Thr Leu Ala Lys Gln Lys Gly Gly Thr Asp
795 770 775 780

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/088,549

DATE: 04/08/2002
TIME: 14:28:32

Input Set : A:\DEBE007US.txt
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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:723 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
M:340 Repeated in SeqNo=6